

73893

STIC-Biotech/ChemLib

Fr m: Yaen, Christopher  
Sent: Wednesday, August 21, 2002 5:51 PM  
To: STIC-Biotech/ChemLib  
Subject: 09811118

could you please run a seq search on seq id no 1 and 2 both regular and oligo

thanks

Christopher Yaen  
Patent Examiner  
US PTO  
Art Unit 1642  
CM1-Rm 8E18  
Mail Box 8E12  
703-305-3586

CRIE

Point of Contact:  
Toby Port  
Technical Info. Specialist  
CM1 6A04  
703-308-3534

Searcher: \_\_\_\_\_  
Phone: \_\_\_\_\_  
Location: \_\_\_\_\_  
Date Picked Up: 8/23  
Date Completed: 8/26  
Searcher Prep/Review: \_\_\_\_\_  
Clerical: \_\_\_\_\_  
Online time: \_\_\_\_\_

TYPE OF SEARCH:  
NA Sequences: 2  
AA Sequences: 2  
Structures: \_\_\_\_\_  
Bibliographic: \_\_\_\_\_  
Litigation: \_\_\_\_\_  
Full text: \_\_\_\_\_  
Patent Family: \_\_\_\_\_  
Other: \_\_\_\_\_

VENDOR/COST (where applic.)  
STN: \_\_\_\_\_  
DIALOG: \_\_\_\_\_  
Questel/Orbit: \_\_\_\_\_  
DRLink: \_\_\_\_\_  
Lexis/Nexis: \_\_\_\_\_  
Sequence Sys.: es  
WWW/Internet: \_\_\_\_\_  
Other (specify): \_\_\_\_\_



## RESULT 2

GPO\_SYN3  
ID GPO\_SYN3 STANDARD; PRT; 169 AA.  
AC P74250;  
DT 30-MAY-2000 (Rel. 39, Created)  
DT 30-MAY-2000 (Rel. 39, Last sequence update)  
DT 16-OCT-2001 (Rel. 40, Last annotation update)  
DE Putative glutathione peroxidase (EC 1.11.1.9).  
GN SLR1171.  
OS Synechocystis sp. (strain PCC 6803)  
OC Bacteria; Cyanobacteria; Chroococcales; Synechocystis.  
OX NCBI\_TaxID=1148;  
RN [1]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=97061201; PubMed=8905231;  
RA Kaneo T., Sato S., Kotani H., Tanaka A., Asamizu E., Nakamura Y.,  
RA Miyajima N., Hirosewa M., Sugiyama M., Sasamoto S., Kimura T.,  
RA Hosouchi T., Matsuno A., Muraki A., Nakazaki N., Naito K., Okumura S.,  
RA Shimo S., Takeuchi C., Wada T., Watanabe A., Yamada M., Yasuda M.,  
RA Tabata S.;  
RT "Sequence analysis of the genome of the unicellular cyanobacterium  
RT Synechocystis sp. strain PCC6803. II. Sequence determination of the  
RT entire genome and assignment of potential protein-coding regions.";  
RL DNA Res. 3:109-136(1996).  
CC -1- CATALYTIC ACTIVITY: 2 glutathione + H(2)O(2) = oxidized  
CC glutathione + 2 H(2)O.  
CC -1- SIMILARITY: BELONGS TO THE GLUTATHIONE PEROXIDASE FAMILY.  
CC This SWISS-PROT entry is copyright. It is produced through a collaboration  
CC between the Swiss Institute of Bioinformatics and the EMBL outstation  
CC the European Bioinformatics Institute. There are no restrictions on its  
CC use by non-profit institutions as long as its content is in no way  
CC modified and this statement is not removed. Usage by and for commercial  
CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>  
CC or send an email to [license@sib-sib.ch](mailto:license@sib-sib.ch)).  
CC  
DR EMBL: D90913; BAA18344.1; -  
DR HSSP: P00435; 1GP1.  
DR InterPro: IPR000889; Glut\_peroxidase.  
DR Pfam: PF00255; GSHpx.1.  
DR PRINTS: PRO1011; GLUTPROXADSE.  
DR PROSITE: PS00460; GLUTATHIONE\_PEROXID\_1; 1.  
DR PROSITE: PS00763; GLUTATHIONE\_PEROXID\_2; 1.  
KW Peroxidase; Oxidoreductase; Complete Proteome.  
FT ACT SITE 41  
FT ACT SITE 41  
SO SEQUENCE 169 AA; 18452 MW; 0DC382089CE39E2 CRC64;

Query Match 5.9%; Score 11; DB 1; Length 169;  
Best Local Similarity 100.0%; Pred. No. 0.00069;  
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 84 PFNONGGOEP 94  
DB 67 PFNONGGOEP 77  
IIIIIIIIII

RESULT 3  
GSHD\_CAMEL  
ID GSHD\_CAMEL STANDARD; PRT; 163 AA.  
AC 86327;  
DT 30-MAY-2000 (Rel. 39, Created)  
DT 30-MAY-2000 (Rel. 39, Last sequence update)  
DT 30-MAY-2000 (Rel. 39, Last annotation update)  
DE Probable glutathione peroxidase R05H10.5 (EC 1.11.1.9).  
GN R05H10.5.  
OS Caenorhabditis elegans.  
OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditidae;  
OC Rhabditidae; Peloderinae; Caenorhabditis.  
OX NCBI\_TaxID=6239;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=BRISTOL NZ;  
RA McMurray A.;

RL Submitted (NOV-1996) to the EMBL/GenBank/DBJ databases.  
CC -1- FUNCTION: MAY CONSTITUTE A GLUTATHIONE PEROXIDASE-LIKE  
CC PROTECTIVE SYSTEM AGAINST OXIDATIVE STRESSES (BY SIMILARITY).  
CC -1- CATALYTIC ACTIVITY: 2 glutathione + H(2)O(2) = oxidized  
CC glutathione + 2 H(2)O.  
CC -1- SUBCELLULAR LOCATION: Cytoplasmic (Potential).  
CC -1- SIMILARITY: BELONGS TO THE GLUTATHIONE PEROXIDASE FAMILY.  
CC This SWISS-PROT entry is copyright. It is produced through a collaboration  
CC between the Swiss Institute of Bioinformatics and the EMBL outstation  
CC the European Bioinformatics Institute. There are no restrictions on its  
CC use by non-profit institutions as long as its content is in no way  
CC modified and this statement is not removed. Usage by and for commercial  
CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>  
CC or send an email to [license@sib-sib.ch](mailto:license@sib-sib.ch)).  
CC  
DR EMBL: 283119; CAB05581.1; -  
DR HSSP: P00435; 1GP1.  
DR WormBep: R05H10.5; CE18107.  
DR InterPro: IPR000889; Glut\_peroxidase.  
DR Pfam: PF00255; GSHpx.1.  
DR PRINTS: PRO1011; GLUTPROXADSE.  
DR PROSITE: PS00460; GLUTATHIONE\_PEROXID\_1; 1.  
DR PROSITE: PS00763; GLUTATHIONE\_PEROXID\_2; 1.  
KW Oxidoreductase; Peroxidase.  
FT ACT SITE 36  
FT ACT SITE 36  
SO SEQUENCE 163 AA; 18152 MW; 8D5FE6DF96D212CA CRC64;

Query Match 5.3%; Score 10; DB 1; Length 163;  
Best Local Similarity 100.0%; Pred. No. 0.0072;  
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 81 VLAFCNONG 90  
DB 60 VLAFCNONG 69  
IIIIIIIIII

RESULT 4  
GSHX\_PINPS  
ID GSHX\_PINPS STANDARD; PRT; 17 AA.  
AC P81087;  
DT 15-JUL-1998 (Rel. 36, Created)  
DT 15-JUL-1998 (Rel. 36, Last sequence update)  
DT 30-MAY-2000 (Rel. 39, Last annotation update)  
DE Glutathione peroxidase homolog (EC 1.11.1.9) (water stress responsive  
DE proteins 8 and 9) (fragment).  
OS Pinus pinaster (Maritime pine).  
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
OC Spermatophyta; Coniferales; Pinaceae; Pinus.  
OX NCBI\_TaxID=71647;  
RN [1]  
RP SEQUENCE.  
RC TISSUE=Needle;  
RX MEDLINE=96418576; PubMed=9747804;  
RX Costa P., Bahman N., Frigerio J.-M., Kremer A., Plomion C.;  
RT "Water-deficit-responsive proteins in maritime pine.";  
RL Plant Mol. Biol. 38:587-596(1998).  
RN [2]  
RP SEQUENCE.  
RC TISSUE=Needle;  
RX MEDLINE=99274088; PubMed=10344291;  
RX Costa P., Plomion C., Bauw G., Dubos C., Bahman N., Kremer A.,  
RA Frigerio J.-M., Plomion C.;  
RT "Separation and characterization of needle and xylem maritime pine  
RT proteins.";  
RL Electrophoresis 20:1098-1108(1999).  
CC -1- CATALYTIC ACTIVITY: 2 glutathione + H(2)O(2) = oxidized  
CC glutathione + 2 H(2)O.  
CC -1- INDUCTION: BY WATER STRESS.  
CC -1- MISCELLANEOUS: ON THE 2D-GEL THE DETERMINED PI OF THIS PROTEIN IS:  
CC 5.6 TO 6.7, ITS MW IS: 20 TO 23 KDa.  
CC -1- SIMILARITY: BELONGS TO THE GLUTATHIONE PEROXIDASE FAMILY.

DR HSSP: P00435; 1GP1.  
 DR InterPro: IPR000889; Glut\_peroxidase.  
 DR Pfam: PF00255; GSHpx; 1.  
 DR PROSITE: PS00460; GLUTATHIONE\_PEROXID\_1; PARTIAL.  
 DR PROSITE: PS00763; GLUTATHIONE\_PEROXID\_2; 1.  
 KW Peroxidase; Oxidoreductase.  
 FT NON\_TER 1 17  
 FT 17 17  
 SQ SEQUENCE 17 AA; 1943 MW; 4D245E9B57868C1 CRC64;

Query Match 4.8%; Score 9; DB 1; Length 17;  
 Best Local Similarity 100.0%; Pred. No. 0.01;  
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 82 LAFCPCNOFG 90  
 DB 9 LAFCPCNOFG 17

RESULT 5  
 GSHC\_CAEEL STANDARD; PRT; 163 AA.  
 ID GSHC\_CAEEL 002621;  
 DT 30-MAY-2000 (Rel. 39, Created)  
 DT 30-MAY-2000 (Rel. 39, Last sequence update)  
 DT 30-MAY-2000 (Rel. 39, Last annotation update)  
 DE Probable glutathione peroxidase F26E4.12 (EC 1.11.1.9).  
 GN F26E4.12.  
 OS Caenorhabditis elegans.  
 OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditidae;  
 OC Rhabditidae; Peloderinae; Caenorhabditis.  
 OX NCBI\_TaxID=6239;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN-BRISTOL N2;  
 RA Lightning J.;  
 RL Submitted (OCT-1996) to the EMBL/GenBank/DBJ databases.  
 CC -1- FUNCTION: MAY CONSTITUTE A GLUTATHIONE PEROXIDASE-LIKE  
 CC PROTECTIVE SYSTEM AGAINST OXIDATIVE STRESSES (BY SIMILARITY).  
 CC -1- CATALYTIC ACTIVITY: 2 glutathione + H(2)O(2) = oxidized  
 CC glutathione + 2 H(2)O.  
 CC -1- SUBCELLULAR LOCATION: Cytoplasmic (Potential).  
 CC -1- SIMILARITY: BELONGS TO THE GLUTATHIONE PEROXIDASE FAMILY.  
 CC -----  
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration  
 CC between the Swiss Institute of Bioinformatics and the EMBL outstation -  
 CC the European Bioinformatics Institute. There are no restrictions on its  
 CC use by non-profit institutions as long as its content is in no way  
 CC modified and this statement is not removed. Usage by and for commercial  
 CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>  
 CC or send an email to [license@isb-sib.ch](mailto:license@isb-sib.ch)).  
 CC -----  
 DR EMBL: Z61070; CAB03004.1; -.  
 DR HSSP: P00435; 1GP1.  
 DR WormBep: F26E4.12; CE09696.  
 DR InterPro: IPR000889; Glut\_peroxidase.  
 DR Pfam: PF00255; GSHpx; 1.  
 DR PRINTS: PR01011; GLUTPROXDASE.  
 DR PROSITE: PS00460; GLUTATHIONE\_PEROXID\_1; 1.  
 DR PROSITE: PS00763; GLUTATHIONE\_PEROXID\_2; 1.  
 KW Oxidoreductase; Peroxidase.  
 FT ACT\_SITE 36 36  
 FT 36 36 BY SIMILARITY.  
 SQ SEQUENCE 163 AA; 18424 MW; 441535A92DC4330F CRC64;

Query Match 4.8%; Score 9; DB 1; Length 163;  
 Best Local Similarity 100.0%; Pred. No. 0.078;  
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 OY 81 VLAFCPCNOFG 89  
 DB 60 VLAFCPCNOFG 68

RESULT 6  
 GSHZ\_CITSI STANDARD; PRT; 167 AA.  
 ID GSHZ\_CITSI 00652;  
 DT 01-JUN-1994 (Rel. 29, Created)  
 DT 01-JUN-1994 (Rel. 29, Last sequence update)  
 DT 30-MAY-2000 (Rel. 39, Last annotation update)  
 DE Glutathione peroxidase homolog (EC 1.11.1.9) (Salt-associated  
 DE protein).  
 DE CSA.  
 OS Citrus sinensis (Sweet orange).  
 GN Citrus sinensis (Sweet orange).  
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;  
 OC euroids II; Sapindales; Rutaceae; Citrus.  
 OX NCBI\_TaxID=2711;  
 RN [1]  
 RP SEQUENCE FROM N.A., AND PARTIAL SEQUENCE.  
 RX MEDLINE-93222490; Pubmed-8467085;  
 RA Holland D., Ben-Hayyim G., Faltin Z., Camoin L., Strosberg A.D.,  
 RA Bshdat Y.;  
 RT "Molecular characterization of salt-stress-associated protein in  
 RT citrus: protein and cDNA sequence homology to mammalian glutathione  
 RT peroxidases.";  
 RL Plant Mol. Biol. 21:923-927(1993).  
 CC -1- FUNCTION: MAY CONSTITUTE A GLUTATHIONE PEROXIDASE-LIKE  
 CC PROTECTIVE SYSTEM AGAINST OXIDATIVE STRESSES.  
 CC -1- CATALYTIC ACTIVITY: 2 glutathione + H(2)O(2) = oxidized  
 CC glutathione + 2 H(2)O.  
 CC -1- INDUCTION: BY SALT STRESS.  
 CC -1- SIMILARITY: BELONGS TO THE GLUTATHIONE PEROXIDASE FAMILY.  
 CC -----  
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration  
 CC between the Swiss Institute of Bioinformatics and the EMBL outstation -  
 CC the European Bioinformatics Institute. There are no restrictions on its  
 CC use by non-profit institutions as long as its content is in no way  
 CC modified and this statement is not removed. Usage by and for commercial  
 CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>  
 CC or send an email to [license@isb-sib.ch](mailto:license@isb-sib.ch)).  
 CC -----  
 DR EMBL: X66377; CAA47018.1; -.  
 DR HSSP: P00435; 1GP1.  
 DR InterPro: IPR000889; Glut\_peroxidase.  
 DR Pfam: PF00255; GSHpx; 1.  
 DR PRINTS: PR01011; GLUTPROXDASE.  
 DR PROSITE: PS00460; GLUTATHIONE\_PEROXID\_1; 1.  
 DR PROSITE: PS00763; GLUTATHIONE\_PEROXID\_2; 1.  
 KW Oxidoreductase; Peroxidase.  
 FT ACT\_SITE 41 41  
 FT 41 41 BY SIMILARITY.  
 SQ SEQUENCE 167 AA; 18596 MW; DB6BDDC363F3260 CRC64;

Query Match 4.8%; Score 9; DB 1; Length 167;  
 Best Local Similarity 100.0%; Pred. No. 0.079;  
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 82 LAFCPCNOFG 90  
 DB 66 LAFCPCNOFG 74

RESULT 7  
 GSHC\_SCHMA STANDARD; PRT; 169 AA.  
 ID GSHC\_SCHMA 000277;  
 DT 01-DEC-1992 (Rel. 24, Created)  
 DT 01-DEC-1992 (Rel. 24, Last sequence update)  
 DT 01-MAR-2002 (Rel. 41, Last annotation update)  
 DE Glutathione peroxidase (EC 1.11.1.9) (GPX).  
 GN GPX1.  
 OS Schistosoma mansoni (Blood fluke).  
 OC Eukaryota; Metazoa; Platyhelminthes; Turbellarian Platyhelminths;

OC Rhabdiphora; Eulcithophora; Revertospermatia; Mediocusata;  
 OC Neodermata; Trematoda; Digenea; Strigoida; Schistosomatoidea;  
 OC Schistosomatidae; Schistosoma.  
 OX NCBI\_TaxID=6183;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN-Puerto Rican;  
 RX MEDLINE=92326859; PubMed=1625700;  
 RA Williams D.L., Pierce R.J., Capron A.;  
 RT "Molecular cloning and sequencing of glutathione peroxidase from  
 RT Schistosoma mansoni.";  
 RL Mol. Biochem. Parasitol. 52:127-130(1992).  
 RN [2]  
 RP REVISION TO 43.  
 RA Williams D.L., Pierce R.J., Capron A.;  
 RL Submitted (JUL-2001) to the EMBL/GenBank/DBJ databases.  
 RN [3]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN-NMRI;  
 RX MEDLINE=95203415; PubMed=7895842;  
 RA Mel H., Loverde P.T.;  
 RT "Schistosoma mansoni: cloning the gene encoding glutathione  
 RT peroxidase.";  
 RL Exp. Parasitol. 80:319-322(1995).  
 RN [4]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN-PUERTO RICAN;  
 RX MEDLINE=94171027; PubMed=8125294;  
 RA Roche C., Williams D.L., Khalife J., Lepresle T., Capron A.,  
 RA Pierce R.J.;  
 RT "Cloning and characterization of the gene encoding Schistosoma  
 RT mansoni glutathione peroxidase.";  
 RL Gene 138:149-152(1994).  
 CC -1- CATALYTIC ACTIVITY: 2 glutathione + H(2)O(2) = oxidized  
 CC glutathione + 2 H(2)O.  
 CC -1- COFACTOR: SELENOCYSTEINE. THE ACTIVE-SITE SELENOCYSTEINE IS  
 CC INCUBED BY THE OPAL CODON, UGA.  
 CC -1- INDUCTION: GPX ACTIVITY INCREASES SIGNIFICANTLY AS WORKS MATURE IN  
 CC THEIR HOST AND IS POSITIVELY CORRELATED TO THE RESISTANCE TO  
 CC ANTIOXIDANTS.  
 CC -1- SIMILARITY: BELONGS TO THE GLUTATHIONE PEROXIDASE FAMILY.  
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration  
 CC between the Swiss Institute of Bioinformatics and the EMBL outstation -  
 CC the European Bioinformatics Institute. There are no restrictions on its  
 CC use by non-profit institutions as long as its content is in no way  
 CC modified and this statement is not removed. Usage by and for commercial  
 CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>  
 CC or send an email to [license@isb-sib.ch](mailto:license@isb-sib.ch)).  
 CC -----  
 DR EMBL; M6510; AAA29885.2; ALT. SEQ.  
 DR EMBL; L3762; AAC14468.2; ALT. SEQ.  
 DR EMBL; L14329; AAB08485.2; ALT. SEQ.  
 DR EMBL; L14328; AAB08485.2; JOINED.  
 DR HSSP; P00435; IGPI.  
 DR InterPro; IPR000889; Glut\_peroxidase.  
 DR Pfam; PF00255; GSHPx.1.  
 DR PRINTS; PRO1011; GLUTPROXDAE.  
 DR PROSITE; PS00460; GLUTATHIONE\_PEROXID\_1; 1.  
 DR PROSITE; PS00763; GLUTATHIONE\_PEROXID\_2; 1.  
 DR Oxioreductase; Peroxidase; Selenium; Selenocysteine.  
 FT SE\_CYS 43  
 FT SEQUENCE 169 AA; 19424 MW; 55D87788BF9F8C10 CRC64;

Query Match 4.8%; Score 9; DB 1; Length 169;  
 Best Local Similarity 100.0%; Pred. No. 0.08;  
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 82 LAFCNORF 90  
 ||||||||  
 Db 68 LAFCNORF 76

RESULT 8  
 GSH2\_NICSY  
 ID GSH2\_NICSY STANDARD; PRT; 169 AA.  
 AC P30708;  
 DT 01-APR-1993 (Rel. 25, Last sequence update)  
 DT 01-APR-1993 (Rel. 25, Last sequence update)  
 DT 30-MAY-2000 (Rel. 39, Last annotation update)  
 DE Glutathione peroxidase homolog 6P229 (EC 1.11.1.9).  
 OS Nicotiana glauca (Wood tobacco).  
 CC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
 CC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;  
 CC Asteridae; euasterids I; Solanales; Solanaceae; Nicotiana.  
 OX NCBI\_TaxID=4096;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC TISSUE=Protoplast;  
 RX MEDLINE=92163033; PubMed=1536938;  
 RA Crilqui M.C., Jamet E., Parentier Y., Marbach J., Durr A., Fleck J.;  
 RT "Isolation and characterization of a plant cDNA showing homology to  
 RT animal glutathione peroxidases.";  
 RL Plant Mol. Biol. 18:623-627(1992).  
 CC -1- FUNCTION: MAY CONSTITUTE A GLUTATHIONE PEROXIDASE-LIKE  
 CC PROTECTIVE SYSTEM AGAINST OXIDATIVE STRESSES.  
 CC -1- CATALYTIC ACTIVITY: 2 glutathione + H(2)O(2) = oxidized  
 CC glutathione + 2 H(2)O.  
 CC -1- TISSUE SPECIFICITY: GERMINATING SEED, APEX, FLOWER, AS WELL AS IN  
 CC STRESSED TISSUES.  
 CC -1- SIMILARITY: BELONGS TO THE GLUTATHIONE PEROXIDASE FAMILY.  
 CC -----  
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration  
 CC between the Swiss Institute of Bioinformatics and the EMBL outstation -  
 CC the European Bioinformatics Institute. There are no restrictions on its  
 CC use by non-profit institutions as long as its content is in no way  
 CC modified and this statement is not removed. Usage by and for commercial  
 CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>  
 CC or send an email to [license@isb-sib.ch](mailto:license@isb-sib.ch)).  
 CC -----  
 DR EMBL; X60219; CAA42780.1; -  
 DR PIR; S20501; S20501.  
 DR HSSP; P00435; IGPI.  
 DR InterPro; IPR000889; Glut\_peroxidase.  
 DR Pfam; PF00255; GSHPx.1.  
 DR PRINTS; PRO1011; GLUTPROXDAE.  
 DR PROSITE; PS00460; GLUTATHIONE\_PEROXID\_1; 1.  
 DR PROSITE; PS00763; GLUTATHIONE\_PEROXID\_2; 1.  
 DR Oxioreductase; Peroxidase.  
 FT ACT\_SITE 43  
 FT SEQUENCE 169 AA; 18767 MW; 401919069E1E97C7 CRC64;

Query Match 4.8%; Score 9; DB 1; Length 169;  
 Best Local Similarity 100.0%; Pred. No. 0.08;  
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 82 LAFCNORF 90  
 ||||||||  
 Db 68 LAFCNORF 76

RESULT 9  
 GSHY\_HELAN  
 ID GSHY\_HELAN STANDARD; PRT; 180 AA.  
 AC O23968;  
 DT 15-DEC-1998 (Rel. 37, Created)  
 DT 15-DEC-1998 (Rel. 37, Last sequence update)  
 DT 30-MAY-2000 (Rel. 39, Last annotation update)  
 DE Glutathione peroxidase 2 (EC 1.11.1.9).  
 OS Helianthus annuus (Common sunflower).  
 CC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
 CC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;  
 CC Asteridae; euasterids II; Asterales; Asteraceae; Asteroideae;

OC Helianthae: Helianthus.  
OX NCBI\_TaxID=4232;  
RN SEQUENCE FROM N.A.  
RA Drevet J.R., Gagne G., Touryelle de Labrouhe D., Nicolas P.,  
RL Dufure J.P., Ledoligt G., Roedel-Drevet P.;  
Submitted (Oct-1997) to the EMBL/GenBank/DBJ databases.  
CC -1- FUNCTION: MAY CONSTITUTE A GLUTATHIONE PEROXIDASE-LIKE  
CC PROTECTIVE SYSTEM AGAINST OXIDATIVE STRESSES.  
CC -1- CATALYTIC ACTIVITY: 2 glutathione + H(2)O(2) = oxidized  
CC glutathione + 2 H(2)O.  
CC -1- SIMILARITY: BELONGS TO THE GLUTATHIONE PEROXIDASE FAMILY.  
CC -----  
CC This SWISS-PROT entry is copyright. It is produced through a collaboration  
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -  
CC the European Bioinformatics Institute. There are no restrictions on its  
CC use by non-profit institutions as long as its content is in no way  
CC modified and this statement is not removed. Usage by and for commercial  
CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>  
CC or send an email to [license@isb-sib.ch](mailto:license@isb-sib.ch)).  
CC -----  
DR EMBL: Y14707; CAA75009.1; -.  
DR HSSP: P00435; IGPI.  
DR InterPro: IPR000889; Glut\_peroxidase.  
DR Pfam: PF00255; GSHpx; 1.  
DR PRINTS: PR01011; GLUTPROXDAE.  
DR PROSITE: PS00460; GLUTATHIONE\_PEROXID\_1; 1.  
DR PROSITE: PS00763; GLUTATHIONE\_PEROXID\_2; 1.  
DR Oxidoreductase; Peroxidase.  
KW ACT\_SITE 54 54 BY SIMILARITY.  
FT SEQUENCE 180 AA; 20174 MW; E33090DAAD2ADE0 CRC64;  
SQ  
  
Query Match 4.8%; Score 9; DB 1; Length 180;  
Best Local Similarity 100.0%; Pred. No. 0.085; Indels 0; Gaps 0;  
Matches 9; Conservative 0; Mismatches 0;  
  
OY 82 LAEPCNOFG 90  
DB 79 LAEPCNOFG 87  
  
RESULT 10  
GSHH\_HUMAN  
AC P36969; 043381; STANDARD; PRT; 197 AA.  
DT 01-JUN-1994 (Rel. 29, Created)  
DT 16-OCT-2001 (Rel. 40, Last sequence update)  
DT 01-MAR-2002 (Rel. 41, Last annotation update)  
DE Phospholipid hydroperoxide glutathione peroxidase, mitochondrial  
DE precursor (EC 1.11.1.9) (PHGPx) (GPX-4).  
GN GPX4.  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.  
OX NCBI\_TaxID=9606;  
RN SEQUENCE FROM N.A.  
RP TISSUE-Testis;  
RC MEDLINE=94314239; PubMed=8039723;  
RA Esworthy R.S., Doan K., Doroshov J.H., Chu F.-F.;  
RT "Cloning and sequencing of the cDNA encoding a human testis  
RT phospholipid hydroperoxide glutathione peroxidase.";  
RL Gene 144:317-318(1994).  
RN [2]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=98381025; PubMed=9705830;  
RA Kelter M.J., Montoya M.A.;  
RT "Structural organization of the human selenium-dependent phospholipid  
RT hydroperoxide glutathione peroxidase gene (GPX4): chromosomal  
RT localization to 19p13.3.";  
RL Biochem. Biophys. Res. Commun. 249:53-55(1998).  
RN [3]

RP SEQUENCE FROM N.A.  
RA Lamerdin J.E., McCready P.M., Skowronski E., Adamson A.W.,  
RA Burkhardt-Schultz K., Gordon L., Kyle A., Ramirez M., Stilaugen S.,  
RA Phan H., Velasco N., Ganes J., Dangnan L., Poundstone P.,  
RA Christensen M., Georgescu A., Ayala J., Liu S., Attix C., Andreise T.,  
RA Tranheim M., Amico-Keller G., Coefield J., Duarte S., Lucas S.,  
RA Bruce R., Thomas P., Quan G., Krommiller B., Arellano A.,  
RA Montomery M., Ow D., Nolan M., Trong S., Kobayashi A., Olsen A.O.,  
RA Carraro A.V.;  
Submitted (Feb-1998) to the EMBL/GenBank/DBJ databases.  
CC -1- FUNCTION: COULD PLAY A MAJOR ROLE IN PROTECTING MAMMALS FROM THE  
CC TOXICITY OF INGESTED LIPID HYDROPEROXIDES.  
CC -1- CATALYTIC ACTIVITY: 2 glutathione + H(2)O(2) = oxidized  
CC glutathione + 2 H(2)O.  
CC -1- COFACTOR: SELENOCYSTEINE. THE ACTIVE-SITE SELENOCYSTEINE IS  
CC ENCODED BY THE OPAL CODON, UGA.  
CC -1- SUBCELLULAR LOCATION: Mitochondrial and cytoplasmic.  
CC -1- ALTERNATIVE PRODUCTS: A SINGLE NUCLEAR GENE PRODUCES BOTH FORMS  
CC BY USE OF ALTERNATIVE INITIATION CODONS IN THE SAME READING FRAME.  
CC -1- TISSUE SPECIFICITY: PRESENT PRIMARILY IN TESTIS.  
CC -1- SIMILARITY: BELONGS TO THE GLUTATHIONE PEROXIDASE FAMILY.  
CC -----  
CC This SWISS-PROT entry is copyright. It is produced through a collaboration  
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -  
CC the European Bioinformatics Institute. There are no restrictions on its  
CC use by non-profit institutions as long as its content is in no way  
CC modified and this statement is not removed. Usage by and for commercial  
CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>  
CC or send an email to [license@isb-sib.ch](mailto:license@isb-sib.ch)).  
CC -----  
DR EMBL: X71973; CAA50793.1; ALT\_SEQ.  
DR EMBL: AF060972; AAC32261.1; ALT\_SEQ.  
DR EMBL: AC004151; AAC03239.1; ALT\_SEQ.  
DR HSSP: P00435; IGPI.  
DR MIM: 138322; -.  
DR InterPro: IPR000889; Glut\_peroxidase.  
DR Pfam: PF00255; GSHpx; 1.  
DR PRINTS: PR01011; GLUTPROXDAE.  
DR PROSITE: PS00460; GLUTATHIONE\_PEROXID\_1; 1.  
DR PROSITE: PS00763; GLUTATHIONE\_PEROXID\_2; 1.  
DR Oxidoreductase; Peroxidase; Selenium; Selenocysteine;  
KW Mitochondrion; Transl peptide; Alternative initiation.  
FT TRANSIT 1 197 MITOCHONDRION (POTENTIAL).  
FT CHAIN 28 197 PHOSPHOLIPID HYDROPEROXIDE GLUTATHIONE  
FT FT SE\_CYS 73 73 PEROXIDASE, MITOCHONDRIAL ISOFORM.  
FT CHAIN 28 197 PHOSPHOLIPID HYDROPEROXIDE GLUTATHIONE  
FT FT SE\_CYS 73 73 PEROXIDASE, CYTOPLASMIC ISOFORM.  
FT INIT\_MET 28 28 FOR CYTOPLASMIC ISOFORM.  
SQ SEQUENCE 197 AA; 22128 MW; 1AE3A2DAEC8FCBB1 CRC64;  
  
Query Match 4.8%; Score 9; DB 1; Length 197;  
Best Local Similarity 100.0%; Pred. No. 0.092; Indels 0; Gaps 0;  
Matches 9; Conservative 0; Mismatches 0;  
  
OY 82 LAEPCNOFG 90  
DB 98 LAEPCNOFG 106  
  
RESULT 11  
GSHH\_MOUSE  
AC 070325; STANDARD; PRT; 197 AA.  
DT 16-OCT-2001 (Rel. 40, Created)  
DT 16-OCT-2001 (Rel. 40, Last sequence update)  
DT 16-OCT-2001 (Rel. 40, Last annotation update)  
DE Phospholipid hydroperoxide glutathione peroxidase, mitochondrial  
DE precursor (EC 1.11.1.9) (PHGPx) (GPX-4).  
GN GPX4.  
OS Mus musculus (Mouse).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Query Match	4.8%	Score 9	DB 1	Length 197
Best Local Similarity	100.0%	Pred. No. 0.092		
Matches 9	Conservative 0	Mismatches 0	Indels 0	Gaps 0
Qy 82	LAFCNORG 90			
Db 98	LAFCNORG 106			
RESULT 12				
ID	GSNH_PIG	STANDARD	PRT	197 AA.
AC	P36968			
DT	01-JUN-1994	(Rel. 29, Created)		
DT	16-OCT-2001	(Rel. 40, Last sequence update)		
DT	01-MAR-2002	(Rel. 41, Last annotation update)		
DE	Phospholipid hydroperoxide glutathione peroxidase, mitochondrial precursor (EC 1.11.1.9) (PHEPX) (GPX-4).			
DE	GPX4.			
NS	Sus scrofa (pig).			

CC	Eukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC	Mammalia, Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
OX	NCBI_TaxID=9623;
RN	[1]
RP	SEQUENCE FROM N.A.
RX	MEDLINE=93312346; PubMed=8323565;
RA	Sunde R.A., Dyer J.A., Moran T., Evenson J.K., Sugimoto M.;
RT	"Phospholipid hydroperoxide glutathione peroxidase: full-length pig
RL	blastocyst cDNA sequence and regulation by selenium status.";
RN	Biochem. Biophys. Res. Commun. 193:905-911(1993).
RN	[2]
RP	SEQUENCE FROM N.A., AND PARTIAL SEQUENCE.
RC	TISSUE=Liver; and Heart;
RX	MEDLINE=94171752; PubMed=8129551;
RA	Brigelius-Flohe R., Annann K.-D., Bloecher H., Gross G.,
RA	Kloepffel E., Flohe L.,
RA	Wiegand E., Flohe L.;
RT	"Phospholipid-hydroperoxide glutathione peroxidase. Genomic DNA,
RT	cDNA, and deduced amino acid sequence.";
RL	J. Biol. Chem. 269:7342-7348(1994).
RN	[3]
RP	SEQUENCE OF 40-197 FROM N.A., AND PARTIAL SEQUENCE.
RC	TISSUE=Heart;
RX	MEDLINE=92137773; PubMed=1778506;
RA	Schuckelt R., Brigelius-Flohe R., Majorino M., Roveri A., Reumkens J.,
RA	Strassburger W., Ursini F., Wolf B., Flohe L.;
RT	"Phospholipid hydroperoxide glutathione peroxidase is a selenoenzyme
RT	distinct from the classical glutathione peroxidase as evident from
RT	cDNA and amino acid sequencing.";
RL	Free Radic. Res. Commun. 14:343-361(1991).
CC	-1- FUNCTION: COULD PLAY A MAJOR ROLE IN PROTECTING MAMMALS FROM THE
CC	TOXICITY OF INGESTED LIPID HYDROPEROXIDES.
CC	-1- CATALYTIC ACTIVITY: 2 glutathione + H(2)O(2) = oxidized
CC	glutathione + 2 H(2)O.
CC	-1- COFACTOR: SELENOCYSTEINE. THE ACTIVE-SITE SELENOCYSTEINE IS
CC	ENCODED BY THE OPAL CODON, USA.
CC	-1- SUBUNIT: MONOMER.
CC	-1- SUBCELLULAR LOCATION: Mitochondrial and cytoplasmic.
CC	-1- ALTERNATIVE PRODUCTS: A SINGLE NUCLEAR GENE PRODUCES BOTH FORMS
CC	BY USE OF ALTERNATIVE INITIATION CODONS IN THE SAME READING FRAME.
CC	-1- SIMILARITY: BELONGS TO THE GLUTATHIONE PEROXIDASE FAMILY.
CC	-----
CC	This SWISS-PROT entry is copyright. It is produced through a collaboration
CC	between the Swiss Institute of Bioinformatics and the EMBL Outstation -
CC	the European Bioinformatics Institute. There are no restrictions on its
CC	use by non-profit institutions as long as its content is in no way
CC	modified and this statement is not removed. Usage by and for commercial
CC	entities requires a license agreement (see <a href="http://www.isb-sib.ch/announce/or_send_an_email_to_license@lsb-sib.ch">http://www.isb-sib.ch/announce/</a>
CC	or send an email to <a href="mailto:license@lsb-sib.ch">license@lsb-sib.ch</a> ).
CC	-----
DR	EMBL, L12743; AAA3109.2; -;
DR	EMBL, L12743; AAA3109.2; ALT_SEQ.
DR	EMBL, X76009; CAAS3596.1; ALT_INT.
DR	EMBL, X76008; CAAS3595.1; ALT_INT.
DR	EMBL, S80257; AAB21327.2; -;
DR	PIR, JN0608; JN0608.
DR	HSSP, P00435; 1GP1.
DR	InterPro: IPR000889; Glut_peroxidase.
DR	Pfam: PF00255; GSHpx. 1.
DR	PRINTS, PR0101; GLUTPEROXIDASE.
DR	PROSITE, PS00460; GLUTATHIONE_PEROXID_1; 1.
DR	PROSITE, PS00763; GLUTATHIONE_PEROXID_2; 1.
DR	Oxidoreductase; Peroxidase; Selenium; Selenocysteine;
KW	Mitochondriac; Transit peptide; Alternative initiation.
FT	TRANSIT 1 ?
FT	CHAIN ? 197
FT	CHAIN 28 197
FT	INTL_MET 28 73
FT	SE_CYS 73
SO	SEQUENCE 197 AA; 22290 MW; 348645ABE35A7FD0 CRC64;



Query Match 4.8%; Score 9; DB 1; Length 197;  
 Best Local Similarity 100.0%; Pred. No. 0.092;  
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 82 LAEPNCFG 90  
 Db 98 LAEPNCFG 106

## RESULT 13

GSNH\_RAT STANDARD; PRT; 197 AA.  
 AC P36970;  
 DT 01-JUN-1994 (Rel. 29, Created)  
 DT 16-OCT-2001 (Rel. 40, Last sequence update)  
 DT 01-MAR-2002 (Rel. 41, Last annotation update)  
 DE Phospholipid hydroperoxide glutathione peroxidase, mitochondrial precursor (EC 1.11.1.9) (PAGPX) (GPX-4).  
 GN GPX4.  
 OS Rattus norvegicus (Rat).  
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sclurognathi; Muridae; Murinae; Rattus.  
 OX NCBI\_TaxID=10116;  
 RN [1]  
 RP SEQUENCE OF 21-197 FROM N.A.  
 RC STRAIN-SPRAGUE-DAWLEY; TISSUE-Liver;  
 RA Sunde R.A., Dyer J.A., Moran T.V., Evenson J.K.;  
 RT "Rat liver phospholipid hydroperoxide glutathione peroxidase.";  
 RL Submitted (Oct-1993) to the EMBL/Genbank/DBJ databases.  
 RN [2]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN-SPRAGUE-DAWLEY; TISSUE-Testis;  
 RX MEDLINE=96070797; PubMed=7592947;  
 RA Puspapa-Rekha T.R., Burdall A.L., Oleksa L.M., Chisolm G.M., Driscoll D.M.;  
 RT "Rat phospholipid-hydroperoxide glutathione peroxidase. cDNA cloning and identification of multiple transcription and translation start sites.";  
 RL J. Biol. Chem. 270:26993-26999(1995).  
 RN [3]  
 RP SEQUENCE OF 17-197 FROM N.A.  
 RC STRAIN-SPRAGUE-DAWLEY; TISSUE-Brain;  
 RX MEDLINE=96318522; PubMed=8749327;  
 RA Imai H., Sumi D., Hanamoto A., Arai M., Sugiyama A., Chiba N., Kuchino Y., Nakagawa Y.;  
 RT "Molecular cloning and functional expression of a cDNA for rat phospholipid hydroperoxide glutathione peroxidase: 3'-untranslated region of the gene is necessary for functional expression.";  
 RL J. Biochem. 118:1061-1067(1995).  
 RN [4]  
 RP CHARACTERIZATION.  
 RC TISSUE-Testis;  
 RA MEDLINE=92210587; PubMed=1556123;  
 RX Koveri A., Casasco A., Maiorino M., Dalan P., Calligaro A., Ursini F.;  
 RT "Phospholipid hydroperoxide glutathione peroxidase of rat testis. Gonadotropin dependence and immunocytochemical identification.";  
 RL J. Biol. Chem. 267:6142-6146(1992).  
 CC -1- FUNCTION: COULD PLAY A MAJOR ROLE IN PROTECTING MAMMALS FROM THE TOXICITY OF INGESTED LIPID HYDROPEROXIDES.  
 CC -1- CATALYTIC ACTIVITY: 2 glutathione + H(2)O(2) = oxidized glutathione + 2 H(2)O.  
 CC -1- COFACTOR: SELENOCYSTEINE. THE ACTIVE-SITE SELENOCYSTEINE IS ENCODED BY THE OPAL CODON, UGA.  
 CC -1- SUBCELLULAR LOCATION: Mitochondrial and cytoplasmic.  
 CC -1- ALTERNATIVE PRODUCTS: A SINGLE NUCLEAR GENE PRODUCES BOTH FORMS BY USE OF ALTERNATIVE INITIATION CODONS IN THE SAME READING FRAME.  
 CC -1- TISSUE SPECIFICITY: PRESENT PRIMARILY IN TESTIS.  
 CC -1- SIMILARITY: BELONGS TO THE GLUTATHIONE PEROXIDASE FAMILY.  
 CC -----  
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its

CC use by non-profit institutions as long as its content is in no way  
 CC modified and this statement is not removed. Usage by and for commercial  
 CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>  
 CC or send an email to [license@isb-sib.ch](mailto:license@isb-sib.ch)).  
 CC -----

DR EMBL: U24896; AAA1842.2; ALT\_INIT.  
 DR EMBL: U37427; AAC52503.1; -  
 DR EMBL: X82679; CAA57996.1; ALT\_INIT.  
 DR HSSP: P00435; IGPI.  
 DR InterPro: IPR000889; Glut\_peroxidase.  
 DR Pfam: PF00255; GSHpx.1.  
 DR PRINTS: PR01011; GLUTPEROXDASE.  
 DR PROSITE: PS00460; GLUTATHIONE\_PEROXID\_1; 1.  
 DR PROSITE: PS00763; GLUTATHIONE\_PEROXID\_2; 1.  
 KW Oxidoreductase; peroxidase; selenium; selenocysteine;  
 KW Mitochondrion; Transil peptide; Alternative initiation.  
 FT TRANSIT 1 197  
 FT CHAIN ? 197  
 FT CHAIN 28 197  
 FT INIT\_MET 28 28  
 FT SEL\_CYS 73 73  
 FT CONFLICT 45 45  
 FT SEQUENCE 197 AA; 22178 MW; 83FE1E8A52E2E14 CRC64;  
 A -> S (IN REF. 2).  
 PEROXIDASE, CYTOPLASMIC ISOFORM.  
 PHOSPHOLIPID HYDROPEROXIDE GLUTATHIONE  
 PEROXIDASE, MITOCHONDRIAL ISOFORM.  
 PHOSPHOLIPID HYDROPEROXIDE GLUTATHIONE  
 PEROXIDASE, CYTOPLASMIC ISOFORM.

Query Match 4.8%; Score 9; DB 1; Length 197;  
 Best Local Similarity 100.0%; Pred. No. 0.092;  
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 82 LAEPNCFG 90  
 Db 98 LAEPNCFG 106

## RESULT 14

GSNH\_ARATH STANDARD; PRT; 242 AA.  
 AC P52032;  
 DT 01-OCT-1996 (Rel. 34, Created)  
 DT 01-OCT-1996 (Rel. 34, Last sequence update)  
 DT 01-MAR-2002 (Rel. 41, Last annotation update)  
 DE Glutathione peroxidase homolog, chloroplast precursor (EC 1.11.1.9).  
 OS Arabidopsis thaliana (Mouse-ear cress).  
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;  
 OC eurosids II; Brassicales; Brassicaceae; Arabidopsis.  
 OX NCBI\_TaxID=3702;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN-CV, COLUMBIA;  
 RA Gachotte D., Benveniste P.;  
 RT "Cloning and sequencing of a glutathione peroxidase homologue from Arabidopsis thaliana.";  
 RL (in) Plant Gene Register PCR95-133.  
 CC -1- CATALYTIC ACTIVITY: 2 glutathione + H(2)O(2) = oxidized glutathione + 2 H(2)O  
 CC -1- SIMILARITY: BELONGS TO THE GLUTATHIONE PEROXIDASE FAMILY.  
 CC -----  
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration  
 CC between the Swiss Institute of Bioinformatics and the EMBL outstation -  
 CC the European Bioinformatics Institute. There are no restrictions on its  
 CC use by non-profit institutions as long as its content is in no way  
 CC modified and this statement is not removed. Usage by and for commercial  
 CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>  
 CC or send an email to [license@isb-sib.ch](mailto:license@isb-sib.ch)).  
 CC -----  
 DR EMBL: X89866; CAA61965.1; -  
 DR HSSP: P00435; IGPI.  
 DR InterPro: IPR000889; Glut\_peroxidase.  
 DR Pfam: PF00255; GSHpx.1.  
 DR PRINTS: PR01011; GLUTPEROXDASE.

DR PROSITE; PS00460; GLUTATHIONE\_PEROXID\_1; 1.  
 DR PROSITE; PS00763; GLUTATHIONE\_PEROXID\_2; 1.  
 KW Peroxidase; Oxidoreductase; Transit peptide; Chloroplast.  
 FT TRANSIT 1 64 CHLOROPLAST (POTENTIAL).  
 FT CHAIN 65 242 GLUTATHIONE\_PEROXIDASE HOMOLOG.  
 FT ACT\_SITE 111 111 BY SIMILARITY.  
 SQ SEQUENCE 242 AA; 26814 MW; 3A7031CCB416B857 CRC64;

Query Match 4.8%; Score 9; DB 1; Length 242;  
 Best Local Similarity 100.0%; Pred. No. 0.11;  
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 82 LAFPNCQFG 90  
 |||||  
 Db 136 LAFPNCQFG 144

Query Match 4.3%; Score 8; DB 1; Length 221;  
 Best Local Similarity 100.0%; Pred. No. 1.1;  
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 82 LAFPNCQF 89  
 |||||  
 Db 96 LAFPNCQF 103

Search completed: August 23, 2002, 14:42:08  
 Job time: 130 sec

RESULT 15  
 GSHU\_DIRIM STANDARD; PRT; 221 AA.  
 AC PS2033;  
 DT 01-OCT-1996 (Rel. 34, Created)  
 DT 01-OCT-1996 (Rel. 34, Last sequence update)  
 DT 01-MAR-2002 (Rel. 41, Last annotation update)  
 DE Glutathione peroxidase precursor (EC 1.11.1.9) (D129).  
 OS Dicrofilaria immitis (Canine heartworm).  
 OC Eukaryota; Metazoa; Nematoda; Chromadorea; Splirurida; Filarioidea;  
 OC Onchocercidae; Dicrofilaria.  
 OX NCBI\_TaxID=6287;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RA Venkatakrisnahalah L., James E.;  
 RL Submitted (JAN-1994) to the EMBL/GenBank/DBJ databases.  
 RN [2]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=98162489; PubMed=9501847;  
 RA Tripp C.A., Frank R.S., Selkirk M.E., Tang L., Mika-Grieve M.,  
 RA Frank G.R., Grieve R.B.;  
 RT "Dicrofilaria immitis: molecular cloning and expression of a cDNA  
 encoding a selenium-independent secreted glutathione peroxidase.",  
 RL Exp. Parasitol. 88:43-50(1998).  
 CC -1- CATALYTIC ACTIVITY: 2 glutathione + H(2)O(2) = oxidized  
 glutathione + 2 H(2)O.  
 CC -1- SUBUNIT: HOMOTETRAMER (BY SIMILARITY).  
 CC -1- SUBCELLULAR LOCATION: Extracellular (By similarity).  
 CC -1- SIMILARITY: BELONGS TO THE GLUTATHIONE\_PEROXIDASE FAMILY.  
 CC -----  
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration  
 CC between the Swiss Institute of Bioinformatics and the EMBL outstation -  
 CC the European Bioinformatics Institute. There are no restrictions on its  
 CC use by non-profit institutions as long as its content is in no way  
 CC modified and this statement is not removed. Usage by and for commercial  
 CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>  
 CC or send an email to [license@isb-sib.ch](mailto:license@isb-sib.ch)).  
 CC -----  
 DR EMBL; U04693; AAA16224.1; -;  
 DR EMBL; U87457; AAB58573.1; -;  
 DR EMBL; U87458; AAB58574.1; -;  
 DR HSSP; P00435; 1GPI  
 DR InterPro; IPR000889; Glut\_peroxidase.  
 DR Pfam; PF00255; GSHpx; 1.  
 DR PRINTS; PR01011; GLUTPROXDASE.  
 DR PROSITE; PS00460; GLUTATHIONE\_PEROXID\_1; 1.  
 DR PROSITE; PS00763; GLUTATHIONE\_PEROXID\_2; 1.  
 KW Oxidoreductase; Peroxidase; Glycoprotein; Signal.  
 FT SIGNAL 1 19 POTENTIAL.  
 FT CHAIN 20 221 GLUTATHIONE\_PEROXIDASE.  
 FT ACT\_SITE 72 72 BY SIMILARITY.  
 FT CARBOHYD 28 28 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 FT CARBOHYD 87 87 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 FT CARBOHYD 90 90 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 SQ SEQUENCE 221 AA; 25453 MW; 88FF848D567CF28 CRC64;



